REMARKS

AMENDMENTS

Claims 1 and 7 are amended herein to limit the variants of the metK and bioS genes to those sequences having from 80-100% homology with the corresponding sequences as given in the sequence listing. Further, the variants are specifically required to show the corresponding enzymatic activity. As the examiner has searched and examined the previously amended claims, in which homologies of up to 50% were claimed, it is reasonable to assume that the present range of variants has also been searched and examined. Accordingly, entry of the present amendments will present no additional burden to the examiner. Applicants respectfully request that these amendments be entered, and that the case be passed to allowance.

RESTRICTION REQUIREMENT

Applicants continue to disagree with the examiner's assessment concerning unity of invention and have petitioned the commissioner on this matter in a petition of even date herewith.

REJECTIONS UNDER 35 USC §112, ¶1

The examiner rejects claims 1 and 3-6 under 35 USC §112, ¶1 for lack of enablement and written description. These rejections are again respectfully traversed.

The present claims are drawn to a process for producing biotin comprising expression of a SAM synthase gene (SEQ ID NO:1) and one or more biotin biosynthesis genes bioS1-3 (SEQ ID NOs 3, 5, and 7), or variants of these four genes having at least 80% homology therewith, in a host organism able to synthesize biotin. It

is intended by the specification disclosure at p.5:11-15 that the term "variants" encompass all variants, functional equivalents, functional analogues, and derivatives as set forward on pages 5-6. Accordingly, the homology restriction applies to each of these possible variants of the four genes. Whether the variant employed is a truncated sequence, a eukaryotic homolog, or any other variant contemplated by the specification disclosure, the present claims require that it have at least 80% homology with the corresponding sequence in the present sequence listing and display the corresponding enzymatic activity.

Applicants respectfully submit that the level of skill in the art is such that the present disclosure, coupled with art-recognized knowledge, is sufficient to enable one of ordinary skill in the art to make and use the entire range of claimed processes. In particular, the homology range allows for some modification of the sequences from those specified in the sequence listing, and yet the amount of modification allowed is within an acceptable range. One of skill in the art would not be unduly burdened in using art-recognized techniques to successfully create structural homologs of the disclosed genes which exhibit the required enzymatic activities.

Additionally, claim 1 recites a process in which the metK and bioS genes are introduced into a host organism "which is able to synthesize biotin." Therefore, "co-expression [in] a host cell not capable of biotin production" is not included therein (office action, p.5).

It is respectfully submitted that the presently amended claims are fully enabled by the present specification in combination with information readily available in the art.

Further, the foregoing remarks apply equally to the rejection made based on the written description requirement of §112, ¶1. The present specification describes certain

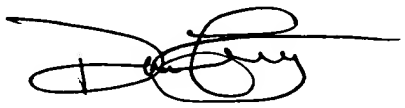
specific variants and a number of general categories of variants. The present claims are limited to those variants which are at least 80% homologous with the provided sequences. One of skill in the art would recognize that such variants were well within the productive capabilities of the applicants at the time of filing. Accordingly, the written description requirement of 35 USC §112, ¶1 has been fulfilled.

CONCLUSION

In view of the present amendments and remarks, applicants consider that the rejections of record have been obviated and respectfully solicit passage of the application to issue.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11-0345. Please credit any excess fees to such deposit account.

Respectfully submitted,
KEIL & WEINKAUF



David C. Liechty
Reg. No. 48,692

1350 Connecticut Ave., N.W.
Washington, D.C. 20036
(202)659-0100

DCL/kas

COPY OF ALL CLAIMS

1. (currently amended) A process for producing biotin wherein an S-adenosylmethionine synthase gene, having the sequence SEQ ID No. 1, and at least one further biotin biosynthesis gene bioS1, bioS2 or bioS3, having the sequences SEQ ID No. 3, SEQ ID No. 5 or SEQ ID No. 7, or functional variants, analogues or derivatives thereof having from 80 to 100% ~~50 to 100%~~ homology based on the corresponding amino acid sequence and possessing the corresponding SAM synthase, bioS1, bioS2, or bioS3 enzymic activity, are expressed in a prokaryotic or eukaryotic host organism which is able to synthesize biotin, this organism is cultured and the synthesized biotin is used directly after separating off the biomass or after purifying the biotin.

2. (canceled)

3. (previously presented) A process as claimed in claim 1, wherein an organism selected from the group of the genera Escherichia, Citrobacter, Serratia, Klebsiella, Salmonella, Pseudomonas, Comamonas, Acinetobacter, Azotobacter, Chromobacterium, Bacillus, Clostridium, Arthrobacter, Corynebacterium, Brevibacterium, Lactococcus, Lactobacillus, Streptomyces, Rhizobium, Agrobacterium, Staphylococcus, Rhodotorula, Sporobolomyces, Yarrowia, Schizosaccharomyces or Saccharomyces is used as the host organism.

4. (previously presented) A process as claimed in claim 1, wherein a regulation-defective biotin mutant is used as the host organism.

5. (previously presented) A process as claimed in claim 1, wherein at least one copy of the genes having the sequences SEQ ID No.1, SEQ ID No. 3, SEQ ID No. 5 and SEQ ID No. 7 as claimed in claim 1 is expressed in a prokaryotic or eukaryotic host organism either alone or together with one or more copies of at least one further biotin gene selected from the group bioA, bioB, bioF, bioC, bioD, bioH, bioP, bioW, bioX, bioY or bioR.

6. (previously presented) A process as claimed in claim 1, wherein at least one copy of the genes having the sequences SEQ ID No.1, SEQ ID No. 3, SEQ ID No. 5 and SEQ ID No. 7 as claimed in claim 1 is expressed in a prokaryotic or eukaryotic host organism either alone or, on a shared vector or on separate vectors, together with one or more copies at least one further biotin gene selected from the group bioA, bioB, bioF, bioC, bioD, bioH, bioP, bioW, bioX, bioY or bioR.

7. (currently amended) A gene construct which comprises an S-adenosylmethionine synthase gene, having the sequence SEQ ID No. 1, and at least one further biotin biosynthesis gene bioS1, bioS2 or bioS3, having the sequences SEQ ID No. 3, SEQ ID No. 5 and SEQ ID No. 7, or their functional variants, analogues or derivatives, which have from 80 to 100% ~~50 to 100%~~ homology based on the corresponding amino acid sequence and possess the corresponding SAM synthase, bioS1, bioS2, or bioS3 enzymic activity, and which is functionally linked to one or more regulatory signals for the purpose of increasing gene expression and/or protein expression and/or whose natural regulation has been switched off.

8. (original) A gene construct as claimed in claim 7, which has been inserted into a vector which is suitable for expressing the gene in a prokaryotic or eukaryotic host organism.

9. (previously presented) A gene construct as claimed in claim 7, wherein the genes having the sequences SEQ ID No. 1, SEQ ID No. 3, SEQ ID No. 5 and SEQ ID No. 7, and also their functional variants, analogues or derivatives, are present in several copies in the gene construct.

10. (previously presented) A gene construct as claimed in claim 7, wherein the S-adenosylmethionine synthase gene, SEQ ID No. 1, and at least one further biotin biosynthesis gene bioS1, bioS2 or bioS3, having the sequences SEQ ID No. 3, SEQ ID No. 5 and SEQ ID No. 7, and also their functional variants, analogues or derivatives, as claimed in claim 7, are present in the gene construct or vector together with one or more copies of at least one further gene selected from the group bioA, bioB, bioF, bioC, bioD, bioH, bioP, bioW, bioX, bioY or bioR.

11. (previously presented) An organism which comprises a gene construct as claimed in claim 7.

12. (canceled)

13. (original) The use of the bioS3 gene, having the sequence SEQ ID No. 7, or of its

functional variants, analogues or derivatives, either alone or in combination with at least one further gene selected from the group S-adenosylmethionine synthase gene, bioS1, bioS2, bioA, bioB, bioF, bioC, bioD, bioH, bioP, bioW, bioX, bioY or bioR, for producing biotin.

14. (previously presented) The use of a gene construct as claimed in claim 7 for producing biotin.

15. (new) A process for producing biotin wherein an S-adenosylmethionine synthase gene having the sequence SEQ ID No. 1, and at least one biotin biosynthesis gene selected from the group consisting of O-acetylserine sufohydrolase A, O-acetylserine sulfohydrolase B, β-cystathionase, nifS, and their prokaryotic and eukaryotic homologues, are expressed in a prokaryotic or eukaryotic host organism which is able to synthesize biotin, this organism is cultured and the synthesized biotin is used directly after separating off the biomass or after purifying the biotin.